Licensable Technologies

GC Buster—Sequencing Through GC-Rich and CCT-Repeat DNA Templates

Application:

- Genomic cDNA sequencing in the life sciences industry and in research institutions

Benefits:

- Ability to sequence genomes accurately from DNA templates with GC-rich regions or CCT repeat regions
- Closing of sequence gaps in human and other organisms where complete data is critical to project success
- Increased quality scores of sequence data collected
- Method easily adapts for existing instrumentation used for PCR-based cycle sequencing
- Allows for sequencing of GC-rich and CCT repeat-rich genomes

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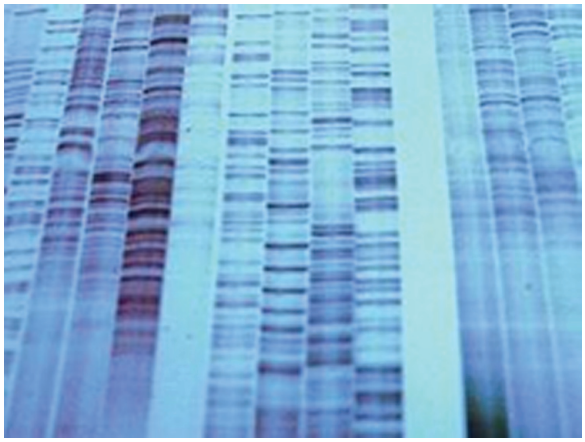

This picture shows 50 or so bases on an autoradiograph of human DNA sequences.

Summary:

Many DNA sequences carry long strands of repeated guanine (G) and cytosine (C) nucleotides. These areas are known to indicate a gene-rich region, that is, a region that would yield invaluable information about the life form containing these nucleotides. Unfortunately for researchers, the GC-rich strands tend to be very tightly coiled, and, therefore, difficult to study, or sequence. Despite ongoing improvements in sequencing chemistries, software, and methods aimed at solving the problems these regions present, no technology has solved these problems successfully up to now. CCT (cytosine-cytosine-thymine)-repeat regions also continue to present similar problems for researchers. Because of difficulties in sequencing both GC-rich regions and CCT-repeat regions, gaps in sequencing projects exist worldwide.

Los Alamos National Laboratory (LANL) has developed a method for generating high-quality sequencing data from GC (guanine-cytosine)-rich (with or without secondary structure) and CCT-repeat regions. Because of problems experienced using standard sequencing methods, a researcher working with LANL's Human Genome Project has invented an effective method for obtaining accurate sequences in these challenging regions.

The new method adapts to widely used sequencing protocols (i.e., PCR-based methods of cycle sequencing DNA), and can be employed when these protocols have failed on GC-rich or CCT-repeat regions. The invention enables genome projects to be completed, and enhances sequencing work in general that has been hindered by GC-rich or CCT-repeat regions.

Development Stage:

This technology is operational and its effectiveness has been demonstrated at LANL.

Patent Status: Patent pending

Licensing Status:

This technology is available for exclusive or non-exclusive licensing.

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